CCCTGTCAGTCTTAAGATTCTAGAAGTCGCTGTCCTATACGGAACCCAAAA
CTCTCACTGTTAATGAAATACCATTGTCGGGGCGAAGATGTAGCTCAGTGGTAAAATACT -121

TGCCAGCACACACAAGAATTAGACTTCAACCGTCACCAACTGCCCTGTGTAGGACGGTCG
GTCACTGAAAGAGAATATTGTCTGCAATACTCTAATGACATCTGTCTGTGTTCATCTGAA -1

SP

1 MetPheHisLeuLysHisSerSerLeuThrValGlyProPheIleSerValMetIleLeu
ATGTTCCATTTAAAACACAGCAGCCTTACTGTTGGACCATTTATCTCAGTAATGATTCTG

▼ ▽

LeuArgPheLeuCysThrGlyArgAsnAsnSerLysGlyArgSerLeuIleGlyArgLeu
CTCCGCTTTCTTTGTACAGGACGCAACAACAGTAAAGGAAGAAGTCTTATTGGCAGATTA 120

41 GluThrGlnProProIleThrGlyLysGlyValProValGluProGlyPheSerIleAsp
GAAACCCAGCCTCCAATCACTGGGAAAGGGGTTCCGGTAGAACCAGGCTTTTCCATCGAT

GluPheSerAlaSerIleLeuThrGlyLysLeuThrThrValPheLeuProValValTyr
GAGTTCTCTGCGTCCATCCTCACCGGGAAGCTGACCACGGTCTTTCTTCCGGTCGTCTAC 240

I

81 IleIleValPheValIleGlyLeuProSerAsnGlyMetAlaLeuTrpIlePheLeuPhe
ATTATTGTGTTTGTGATTGGTTTGCCCAGTAATGGCATGGCCCTCTGGATCTTCCTTTTC

II

ArgThrLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeuAlaAspLeu
CGAACGAAGAAGAAACACCCCGCCGTGATTTACATGGCCAACCTGGCCTTGGCCGACCTC 360

121 LeuSerValIleTrpPheProLeuLysIleSerTyrHisLeuHisGlyAsnAsnTrpVal
CTCTCTGTCATCTGGTTCCCCCTGAAGATCTCCTACCACCTACATGGCAACAACTGGGTC

III

TyrGlyGluAlaLeuCysLysValLeuIleGlyPhePheTyrGlyAsnMetTyrCysSer
TACGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTTTTCTATGGTAACATGTATTGCTCC 480

161 IleLeuPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsnProMetGly
ATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTACTGGGTGATCGTGAACCCCATGGGA

IV

HisProArgLysLysAlaAsnIleAlaValGlyValSerLeuAlaIleTrpLeuLeuIle
CACCCCAGGAAGAAGGCAAACATCGCCGTTGGCGTCTCCTTGGCAATCTGGCTCCTGATT 600

FIG.1A

```
201 PheLeuValThrIleProLeuTyrValMetLysGlnThrIleTyrIleProAlaLeuAsn
    TTTCTGGTCACCATCCCTTTGTATGTCATGAAGCAGACCATCTACATTCCAGCATTGAAC

    IleThrThrCysHisAspValLeuProGluGluValLeuValGlyAsnMetPheAsnTyr
    ATCACCACCTGTCACGATGTGCTGCCTGAGGAGGTATTGGTGGGGGACATGTTCAATTAC 720

                                  V
241 PheLeuSerLeuAlaIleGlyValPheLeuPheProAlaLeuLeuThrAlaSerAlaTyr
    TTCCTCTCACTGGCCATTGGAGTCTTCCTGTTCCCGGCCCTCCTTACTGCATCTGCCTAC

    ValLeuMetIleLysThrLeuArgSerSerAlaMetAspGluHisSerGluLysLysArg
    GTGCTCATGATCAAGACGCTCCGCTCTTCTGCTATGGATGAACACTCAGAGAACAAAAGG 840

                                           VI
281 GlnArgAlaIleArgLeuIleIleThrValLeuAlaMetTyrPheIleCysPheAlaPro
    CAGAGGGCTATCCGACTCATCATCACCGTGCTGGCCATGTACTTCATCTGCTTTCGTCCT

    SerAsnLeuLeuLeuValValHisTyrPheLeuIleLysThrGlnArgGlnSerHisVal
    AGCAACCTTCTGCTCGTAGTGCATTATTTCCTAATCAAAACCCAGAGGCAGAGCCACGTC 960

                                          VII
321 TyrAlaLeuTyrLeuValAlaLeuCysLeuSerThrLeuAsnSerCysIleAspProPhe
    TACGCCCTCTACCTTGTCGCCCTCTGCCTGTCGACCCTCAACAGCTGCATAGACCCCTTT

    ValTyrTyrPheValSerLysAspPheArgAspHisAlaArgAsnAlaLeuLeuCysArg
    GTCTATTACTTTGTCTCAAAAGATTTCAGGGATCACGCCAGAAACGCGCTCCTCTGCCGA 1080

361 SerValArgThrValAsnArgMetGlnIleSerLeuSerSerAsnLysPheSerArgLys
    AGTGTCCGCACTGTGAATCGCATGCAAATCTCGCTCAGCTCCAACAAGTTCTCCAGGAAG
    GATGTCAAGCCTGCTTGATGATGATGATGATGATGGTGTGTGTGTG               1246

    SerGlySerTyrSerSerSerSerThrSerValLysThrSerTyr
    TCCGGCTCCTACTCTTCAAGCTCAACCAGTGTTAAAACCTCCTACTGAGCTGTACCTGAG 1200
```

FIG.1B

```
CGCTCCAGGCCTGGGTGACAGCGAGACCCTGTCTCATAAATTAAAAAATGAATAA

                               SP
MetAsnValLeuSerPheGluGlnThrSerValThrAlaGluThrPheIleSerValMet
ATGAATGTACTTTCATTTGAACAAACCAGTGTTACTGCTGAAACATTTATTTCTGTAATG

ThrLeuValPheLeuSerCysThrGlyThrAsnArgSerSerLysGlyArgSerLeuIle    -1
ACCCTTGTCTTCCTTTCTTGTACAGGAACCAATAGATCCTCTAAAGGAAGAAGCCTTATT   120

GlyLysValAspGlyThrSerHisValThrGlyLysGlyValThrValGluThrValPhe
GGTAAGGTTGATGGCACATCCCACGTCACTGGAAAAGGAGTTACAGTTGAAACAGTCTTT

SerValAspGluPheSerAlaSerValLeuThrGlyLysLeuThrThrValPheLeuPro
TCTGTGGATGAGTTTTCTGCATCTGTCCTCACTGGAAAACTGACCACTGTCTTCCTTCCA   240

                                      I
IleValTyrThrIleValPheValValGlyLeuProSerAsnGlyMetAlaLeuTrpVal
ATTGTCTACACAATTGTGTTTGTGGTGGGTTTGCCAAGTAACGGCATGGCCCTGTGGGTC

PheLeuPheArgThrLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeu
TTTCTTTTCCGAACTAAGAAGAAGCACCCTGCTGTGATTTACATGGCCAATCTGGCCTTG   360

      II
AlaAspLeuLeuSerValIleTrpPheProLeuLysIleAlaTyrHisIleHisGlyAsn
GCTGACCTCCTCTCTGTCATCTGGTTCCCCTTGAAGATTGCCTATCACATACATGGCAAC

AsnTrpIleTyrGlyGluAlaLeuCysAsnValLeuIleGlyPhePheTyrGlyAsnMet
AACTGGATTTATGGGGAAGCTCTTTGTAATGTGCTTATTGGCTTTTTCTATGGCAACATG   480

      III
TyrCysSerIleLeuPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsn
TACTGTTCCATTCTCTTCATGACCTGCCTCAGTGTGCAGAGGTATTGGGTCATCGTGAAC

ProMetGlyHisSerArgLysLysAlaAsnIleAlaIleGlyIleSerLeuAlaIleTrp
CCCATGGGGCACTCCAGGAAGAAGGCAAACATTGCCATTGGCATCTCCCTGGCAATATGG   600
```

FIG.2A

IV
LeuLeuIleLeuLeuValThrIleProLeuTyrValValLysGlnThrIlePheIlePro
CTGCTGATTCTGCTGGTCACCATCCCTTTGTATGTCGTGAAGCAGACCATCTTCATTCCT

AlaLeuAsnIleThrThrCysHisAspValLeuProGluGlnLeuLeuValGlyAspMet
GCCCTGAACATCACGACCTGTCATGATGTTTTGCCTGAGCAGCTCTTGGTGGGAGACATG 720

V
PheAsnTyrPheLeuSerLeuAlaIleGlyValPheLeuPheProAlaPheLeuThrAla
TTCAATTACTTCCTCTCTCTGGCCATTGGGGTCTTTCTGTTCCCAGCCTTCCTCACAGCC

SerAlaTyrValLeuMetIleArgMetLeuArgSerSerAlaMetAspGluAsnSerGlu
TCTGCCTATGTGCTGATGATCAGAATGCTGCGATCTTCTGCCATGGATGAAAACTCAGAG 840

VI
LysLysArgLysArgAlaIleLysLeuIleValThrValLeuAlaMetTyrLeuIleCys
AAGAAAAGGAAGAGGGCCATCAAACTCATTGTCACTGTCCTGGCCATGTACCTGATCTGC

PheThrProSerAsnLeuLeuLeuValValHisTyrPheLeuIleLysSerGlnGlyGln
TTCACTCCTAGTAACCTTCTGCTTGTGGTGCATTATTTTCTGATTAAGAGCCAGGGCCAG 960

VII
SerHisValTyrAlaLeuTyrIleValAlaLeuCysLeuSerThrLeuAsnSerCysIle
AGCCATGTCTATGCCCTGTACATTGTAGCCCTCTGCCTCTCTACCCTTAACAGCTGCATC

AspProPheValTyrTyrPheValSerHisAspPheArgAspHisAlaLysAsnAlaLeu
GACCCCTTTGTCTATTACTTTGTTTCACATGATTTCAGGGATCATGCAAAGAACGCTCTC 1080

LeuCysArgSerValArgThrValLysGlnMetGlnValSerLeuThrSerLysLysHis
CTTTGCCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTATCCCTCACCTCAAAGAAACAC

SerArgLysSerSerSerTyrSerSerSerSerThrThrValLysThrSerTyr *
TCCAGGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTTAAGACCTCCTATTGAGTT 1200

FIG. 2B

```
Mouse C140  M--FHLKHSS LIVGPFISVM ILLRFLCTGR NNSHKGRSLI GRLETQPPIT   47
Human C140  MNVLSFEQTS VTAETFISVM ILVFLSCTGT NRSSKGRSLI GKVDGTSHVT   50

Mouse C140  GKGVFVEPGF SIDEFSASIL TCKLTTVFLP MVYIIVFVIG LPSNGMALWI   97
Human C140  GKGVIVEIVF SMDEFSASVL TGKLTTVFLP IVYIIVFVVG LPSNGMALWV  100

Mouse C140  FLFRTKKKHP AVIYMANLAL ADLLSVIWFP LKISYHLHGN NWMYGEALCK  147
Human C140  FLFRTKKKHP AVIYMANLAL ADLLSVIWFP LKIAYHIHGN NWIYGEALCN  150

Mouse C140  VLIGFFYGNM YCSILFMTCL SVQRYWVIVN PMGHPRKKAN IAMGMSLAIW  197
Human C140  VLIGFFYGNM YCSILFMTCL SVQRYWVIVN PMGHSRKKAN IAIGISLAIW  200

Mouse C140  LLIFLVTIPL YVMKQTIYIP ALNITTCHDV LPEEVLVGDM FNYFLSLAIG  247
Human C140  LLILLVTIPL YVVKQTIPIP ALNITTCHDV LPEQLLVGDM FNYFLSLAIG  250

Mouse C140  VFLFPALLTA SAYVLMIKTL RSSAMDEHSE KKRQRAIRLI ITVLAMYFIC  297
Human C140  VFLFPAFLTA SAYVLMIRML RSSAMDENSE KKRKRAIKLI VTVLAMYLIC  300

Mouse C140  FAPSNLLLVV HYFLIKIQRQ SHVYALYLVA LCLSTLNSCI DPFVYYFVSK  347
Human C140  FIPSNLLLVV HYFLIKSQGQ SHVYALYIVA LCLSTLNSCI DPFVYYFVSH  350

Mouse C140  DFRDHARNAL LCRSVRTVNR MQISLSSNKF SRKSGSYSSS STSVKTSY    395
Human C140  DFRDHAKNAL LCRSVRTVKQ MQMSLISKKH SRKSSSYSSS STTVKTSY    398
```

FIG.3

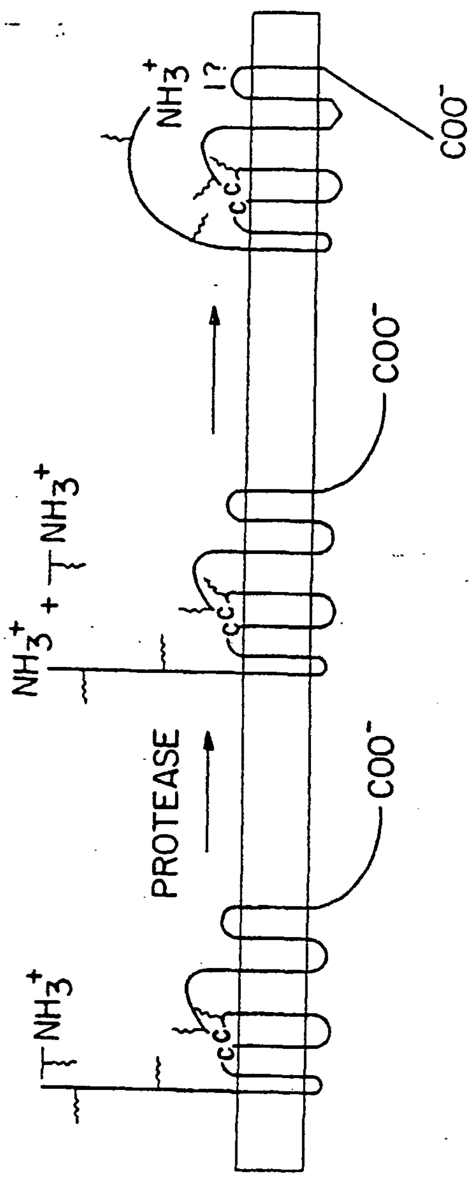

FIG. 4

```
                     SP
C140   MFHLKHSSLTVGPFISVMILLRFLCTGRNNSK-------GRSLIGRLETQP---------  44
HSTHRR MGPRRLLLVAACFSLCGPLLSARTRARRPESKATNATLDPRSFLLRNPNDKYEPEWEDEE  60

                                                                 I
C140   -------------PITGKGVPVEPGFSIDEFSASILTGKLTTVFLPVVYIIVFVIGLPSN  91
HSTHRR KNESGLTEYRLVSINKSSPLQKQLPAFISEDASGYLTSSWLTLFVPSVYTGVFVVSLPLN 120

                                  II
C140   GMALWIFLFRTKKKHPAVIYMANLALADLLSVIWFPLKISYHLHGNNWVYGEALCKVLIG 151
HSTHRR IMAIVVFILKMKVKKPAVVYMLHLATADVLFVSVLPFKISYYFSGSDWQFGSELCRFVTA 180

           III                                         IV
C140   FFYGNMYCSILFMTCLSVQRYWVIVNPM-GHPRKKANIAVGVSLAIWLLIFLVTIPLYVM 210
HSTHRR AFYCNMYASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAIWALAIAGVVPLVLK 240

                                                   V
C140   KQTIYIPALNITTCHDVLPEEVLVGDMFNYFLSLAIGVFLFPALLTASAYVLMIKTLRSS 270
HSTHRR EQTIQVPGLNITTCHDVLNETLLEGYYAYYFSAFSAVFFFVPLIISTVCYVSIIRCLSSS 300

                               VI
C140   AMDEHSEKKRQRAIRLIITVLAMYFICFAPSNLLLVVHY-FLIKTQRQSHVYALYLVALC 329
HSTHRR AVANRSKKSR--ALFLSAAVFCIFIICFGPTNVLLIAHYSFLSHTSTTEAAYFAYLLCVC 358

         VII
C140   LSTLNSCIDPFVYYFVSKDFRDHARNALLCRSVRTVNRMQISLSSNKFSRKSGSYSSSST 389
HSTHRR VSSISSCIDPLIYYYASSECQRYVYSILCCKESSDPSSYNSSGQLMASKMDTCSSNLNNS 418

C140   SVKTSY-                                                      395
HSTHRR IYKKLLT                                                      426
```

FIG.5

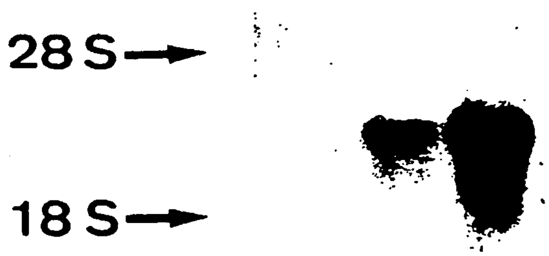

FIG. 6

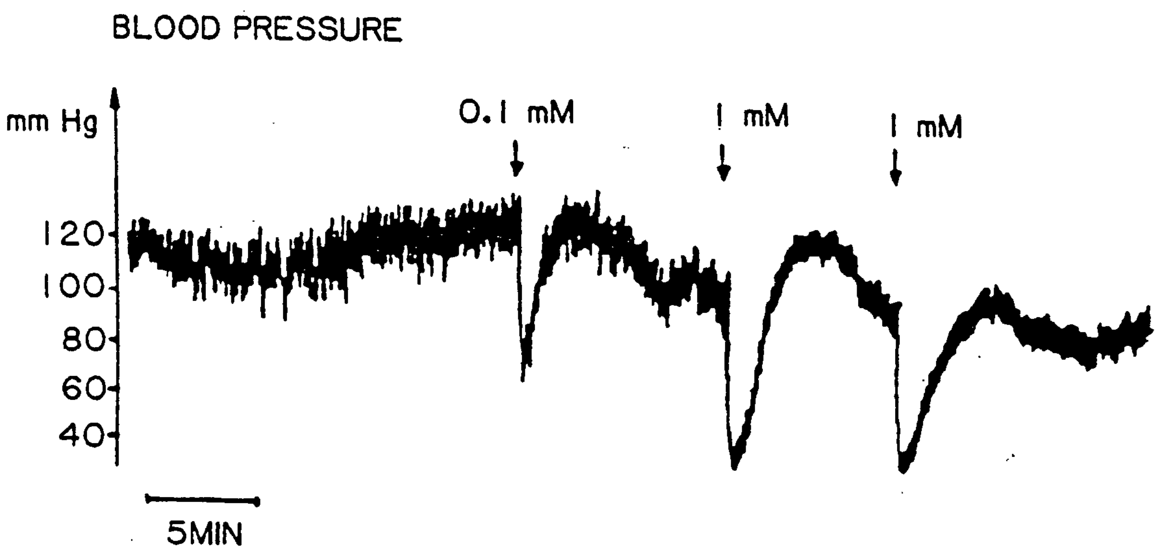

FIG. 7

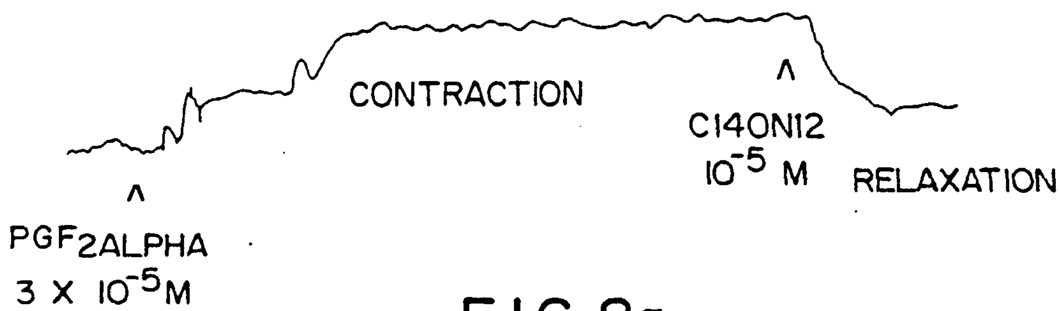
CONTRACTION
C140N12
10-5 M
RELAXATION
PGF2ALPHA
3 X 10-5M

FIG. 8a

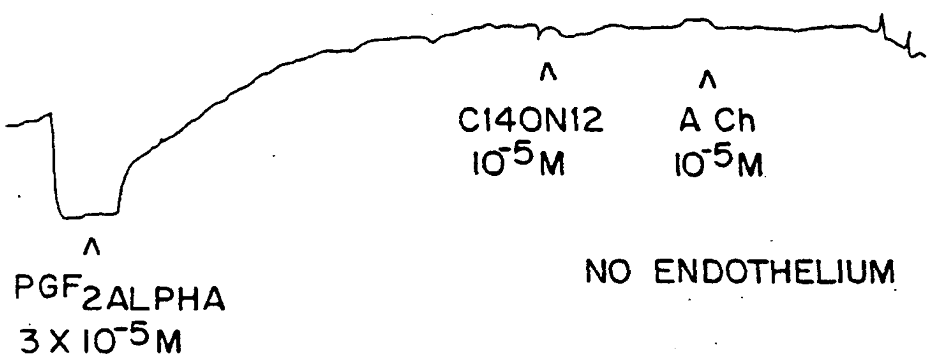
C140N12
10-5M
A Ch
10-5M
PGF2ALPHA
3 X 10-5M
NO ENDOTHELIUM

FIG. 8b

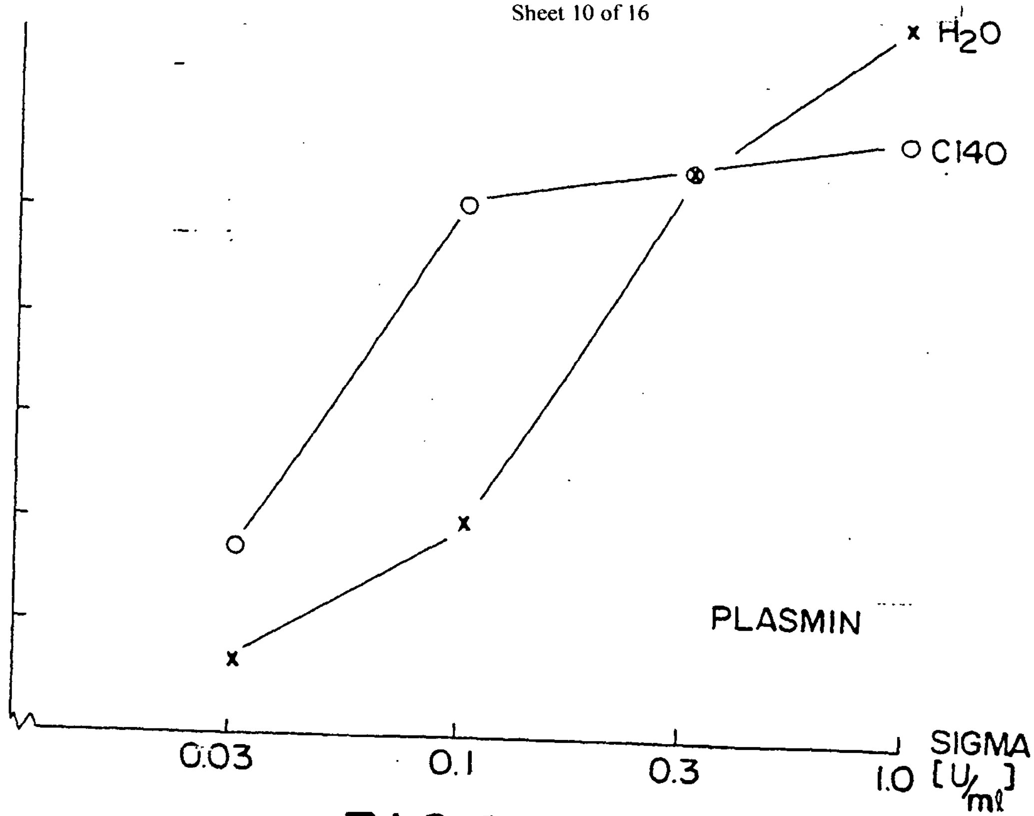
H_2O
C140
PLASMIN
0.03
0.1
0.3
1.0
SIGMA
[U/ml]

FIG. 9a

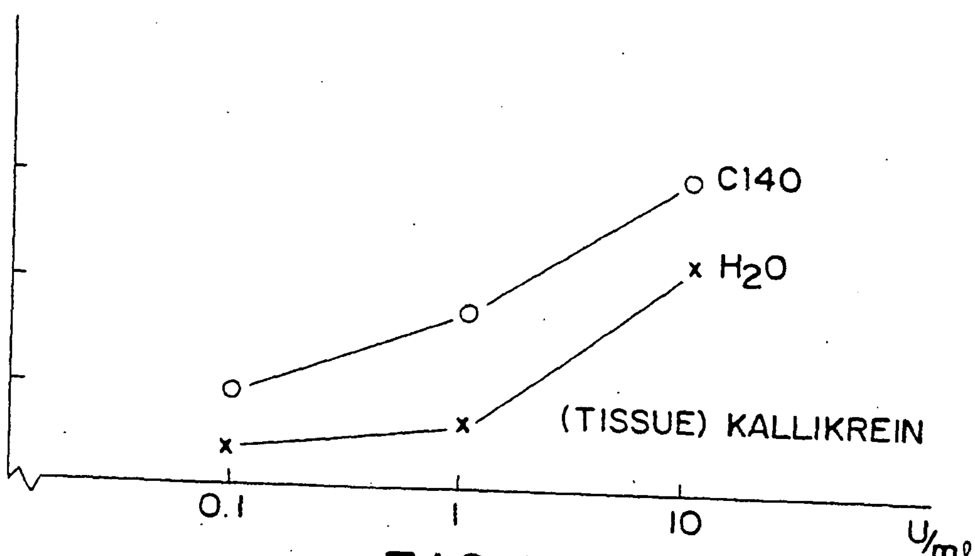
C140
H_2O
(TISSUE) KALLIKREIN
0.1
1
10
U/ml

FIG. 9b

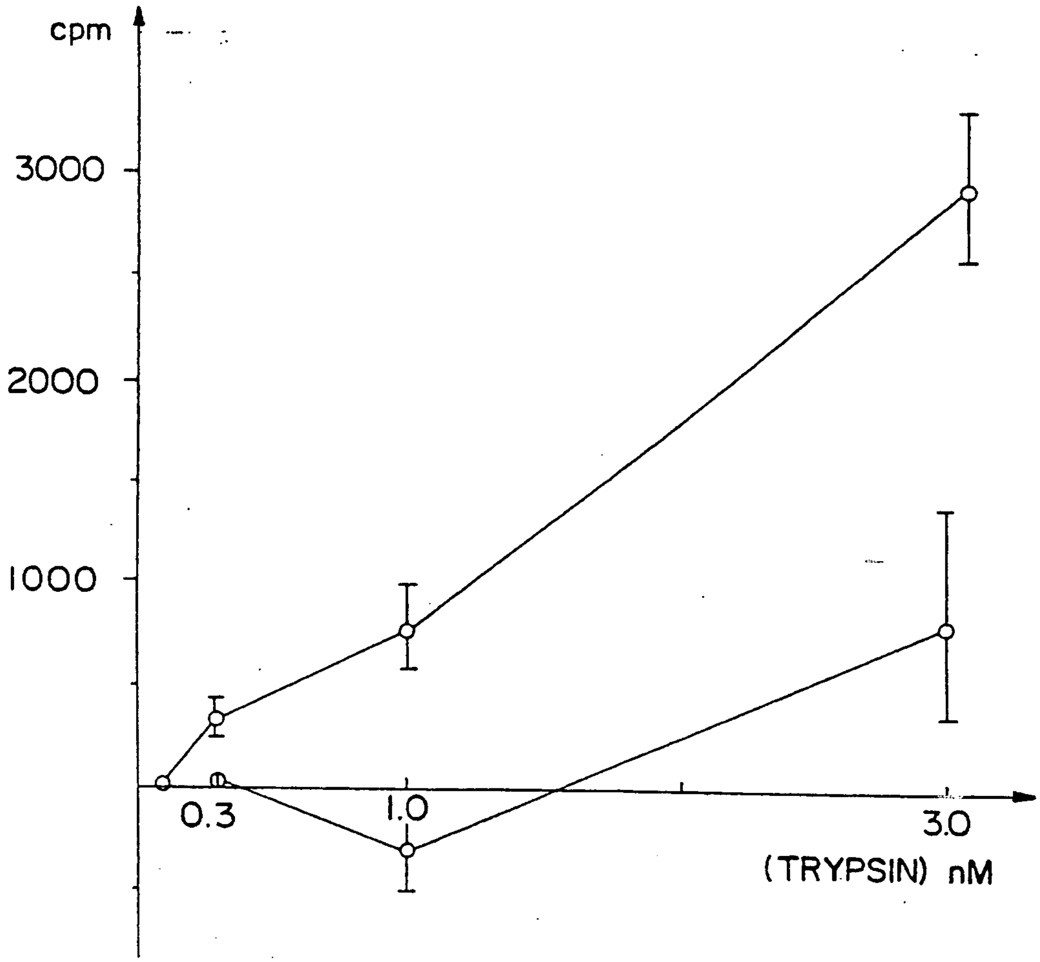

FIG.9c

```
CCCTGTGCTCAGAGTAGGGCTCCGAGTTTCGAACCACTGGTGGCGGATTGCCCGCCCGCC

CCACGTCCGGGGATGCGAAGTCTCAGCCTGGCGTGGCTGCTGGGAGGTATCACCCTTCTG
            M  R  S  L  S  L  A  W  L  L  G  G  I  T  L  L

GCGGCCTCGGTCTCCTGCAGCCGGACCGAGAACCTTGCACCGGGACGCAACAACAGTAAA
A  A  S  V  S  C  S  R  T  E  N  L  A  P  G  R  N  N  S  K

GGAAGAAGTCTTATTGGCAGATTAGAAACCCAGCCTCCAATCACTGGGAAAGGGGTTCCG
G  R  S  L  I  G  R  L  E  T  Q  P  P  I  T  G  K  G  V  P

GTAGAACCAGGCTTTTCCATCGATGAGTTCTCTGCGTCCATCCTCACCGGGAAGCTGACC
V  E  P  G  F  S  I  D  E  F  S  A  S  I  L  T  G  K  L  T

ACGGTCTTTCTTCCGGTCGTCTACATTATTGTGTTTGTGATTGGTTTGCCCAGTAATGGC
T  V  F  L  P  V  V  Y  I  I  V  F  V  I  G  L  P  S  N  G

ATGGCCCTCTGGATCTTCCTTTTCCGAACGAAGAAGAAACACCCCGCCGTGATTTACATG
M  A  L  W  I  F  L  F  R  T  K  K  K  H  P  A  V  I  Y  M

GCCAACCTGGCCTTGGCCGACCTCCTCTCTGTCATCTGGTTCCCCCTGAAGATCTCCTAC
A  N  L  A  L  A  D  L  L  S  V  I  W  F  P  L  K  I  S  Y

CACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTT
H  L  H  G  N  N  W  V  Y  G  E  A  L  C  K  V  L  I  G  F

TTCTATGGTAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTAC
F  Y  G  N  M  Y  C  S  I  L  F  M  T  C  L  S  V  Q  R  Y

TGGGTGATCGTGAACCCCATGGGACACCCCAGGAAGAAGGCAAACATCGCCGTTGGCGTC
W  V  I  V  N  P  M  G  H  P  R  K  K  A  N  I  A  V  G  V

TCCTTGGCAATCTGGCTCCTGATTTTTCTGGTCACCATCCCTTTGTATGTCATGAAGCAG
S  L  A  I  W  L  L  I  F  L  V  T  P  I  L  Y  V  M  K  Q

ACCATCTACATTCCAGCATTGAACATCACCACCTGTCACGATGTGCTGCCTGAGGAGGTA
T  I  Y  I  P  A  L  N  I  T  T  C  H  D  V  L  P  E  E  V

TTGGTGGGGGACATGTTCAATTACTTCCTCTCACTGGCCATTGGAGTCTTCCTGTTCCCG
L  V  G  D  M  F  N  Y  F  L  S  L  A  I  G  V  F  L  F  P

GCCCTCCTTACTGCATCTGCCTACGTGCTCATGATCAAGACGCTCCGCTCTTCTGCTATG
A  L  L  T  A  S  A  Y  V  L  M  I  K  T  L  R  S  S  A  M

GATGAACACTCAGAGAAGAAAAGGCAGAGGGCTATCCGACTCATCATCACCGTGCTGGCC
D  E  H  S  E  K  K  R  Q  R  A  I  R  L  I  I  T  V  L  A

ATGTACTTCATCTGCTTTGCTCCTAGCAACCTTCTGCTCGTAGTGCATTATTTCCTAATC
M  Y  F  I  C  F  A  P  S  N  L  L  L  V  V  H  Y  F  L  I

AAAACCCAGAGGCAGAGCCACGTCTACGCCCTCTACCTTGTCGCCCTCTGCCTGTCGACC
K  T  Q  R  Q  S  H  V  Y  A  L  Y  L  V  A  L  C  L  S  T

CTCAACAGCTGCATAGACCCCTTTGTCTATTACTTTGTCTCAAAAGATTTCAGGGATCAC
L  N  S  C  I  D  P  F  V  Y  Y  F  V  S  K  D  F  R  D  H
```

FIG. 10A

```
GCCAGAAACGCGCTCCTCTGCCGAAGTGTCCGCACTGTGAATCGCATGCAAATCTCGCTC
A  R  N  A  L  L  C  R  S  V  R  T  V  N  R  M  Q  I  S  L

AGCTCCAACAAGTTCTCCAGGAAGTCCGGCTCCTACTCTTCAAGCTCAACCAGTGTTAAA
S  S  N  K  F  S  R  K  S  G  S  Y  S  S  S  S  T  S  V  K

ACCTCCTACTGAGCTGTACCTGAGGATGTCAAGCCTGCTTGATGATGATGATGATGATGG
T  S  Y

TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCACCCGTGTGTGAGTGCGTG

GTAGGGATACACCAACATGGATGGGGCTGTCATTTCCTATCCAAGCTGTCTGTCTCTGCA

CCAATCACAAGCATGCAGCTCTCCCCAGGATTGACAGAAGCCTCCTCCTTTGCATGAGAA

CAGTCTTCCACTCTGATGAAAAGCATCAGTATCAGAAACTGAAACGAACTGAGAGGAGCT

TGTTTTGTGAAAGTGAAGAGAAGATGGAGGGTCAGTGACTTGCAAAAAAAACCAACCAAA

CAAAAACTACACCTGGCAAGAAGGCTAAGACTCTCTGAAATGCTTCCCTTTTCCATCTGG

AGTTCGTCTCGGCCTTGTTCAGGACCTGAGGCCCTGGTAGAGCTTCAGTCCAGTTGATTG

ACTTTACAGACTTGAGAGAGGAGTGAATGAGGAGTGAATGAGGCTCCTGGCGGCATCCTA

ACCGGCTAACAGTGGCCTTGCTGGACAATAGGATTCAGATGGCTGGAGTTACATTCTCAC

ACCATTTCATCAGAACTATTGGGGATCTTGATCAATGTGCAGGTCCCTTAGCGTCAGTAA

CCCTGGGAGCTCAGACACGATGGGGGTGAGGGTGGGGGTGGGGGTGGGGGTGAGGCTCTA

CAAACCTTAGTGATGACTGCAGACACAGAACCATGGAGCTGAGCCTGCTTCTGCTTGCCA

GGGCACCACTGTAATGTTGGCAAAGAAAAACCAACAGCAGTGTTTTGAGCCGTCTTTTTTT

GGTCAGTTTATGATGAATTTGCCTATTGGTTTATTGGGATTTTCAGTTCCTTTATTACTT

TGTTGTAATTTTGTGTGTTTATTAGTCAAGAAAAAGAAGATGAGGCTCTTAAAAATGTAA

ATAAAATTTTTGGTTTTTTGGTTTTTTAACTTGGGCCAACTACAAATACTGCTTAGGTTT

TTTTCTAACTTAATTGTTAACTACATCATGTGAACTTAAGACATTTTCATGATAAAGCAT

TACTGTAGTGTCAGTTTTCCCTCATCCTCGATCATAGTCCTTCCCGTGAAGCAGGGCCCT

TCCCCTCCCCCCCCTTTGCCGTTTCCCTCCCCACCAGATAGTCCCCCTGTCTGCTTTAAC

CTACCAGTTAGTATTTTATAAAAACAGATCATTGGAATATTTATTATCAGTTTTGTTCAC

TTGTTATCAGTTTTGTTCACTAATTTGTCCAATAATGGAATTAACGTCTTCTCATCTGTT

TGAGGAAGATCTGAAACAAGGGGCCATTGCAGGAGTACATGGCTCCAGGCTTACTTTATA

TACTGCCTGTATTTGTGGCTTTAAAAAAATGACCTTGTTATATGAATGCTTTATAAATAA

ATAATGCATGAACTTTAAAAAAAAAAAAAAA
```

FIG. 10B

```
         10        20        30        40        50        60
123456789012345678901234567890123456789012345678901234567890
CAAAGAATTGTAATACGACTCACTATAGGGCGAATTCGGATCCAGGAGGATGCGGAGCCC
                                                 MetArgSerPr

         70        80        90       100       110       120
123456789012345678901234567890123456789012345678901234567890
CAGCGCGGCGTGGCTGCTGGGGGCCGCCATCCTGCTAGCAGCCTCTCTCTCCTGCAGTGG   120
oSerAlaAlaTrpLeuLeuGlyAlaAlaIleLeuLeuAlaAlaSerLeuSerCysSerGl

CACCATCCAAGGAACCAATAGATCCTCTAAAGGAAGAAGCCTTATTGGTAAGGTTGATGG
yThrIleGlnGlyThrAsnArgSerSerLysGlyArgSerLeuIleGlyLysValAspGl

CACATCCCACGTCACTGGAAAAGGAGTTACAGTTGAAACAGTCTTTTCTGTGGATGAGTT   240
yThrSerHisValThrGlyLysGlyValThrValGluThrValPheSerValAspGluPh

TTCTGCATCTGTCCTCGCTGGAAAACTGACCACTGTCTTCCTTCCAATTGTCTACACAAT
eSerAlaSerValLeuAlaGlyLysLeuThrThrValPheLeuProIleValTyrThrIl

TGTGTTTGCGGTGGGTTTGCCAAGTAACGGCATGGCCCTATGGGTCTTTCTTTTCCGAAC   360
eValPheAlaValGlyLeuProSerAsnGlyMetAlaLeuTrpValPheLeuPheArgTh

TAAGAAGAAGCACCCTGCTGTGATTTACATGGCCAATCTGGCCTTGGCTGACCTCCTCTC
rLysLysLysHisProAlaValIleTyrMetAlaAsnLeuAlaLeuAlaAspLeuLeuSe

TGTCATCTGGTTCCCCTTGAAGATTGCCTATCACATACATGGCAACAACTGGATTTATGG   480
rValIleTrpPheProLeuLysIleAlaTyrHisIleHisGlyAsnAsnTrpIleTyrGl

GGAAGCTCTTTGTAATGTGCTTATTGGCTTTTTCTATCGCAACATGTACTGTTCCATTCT
yGluAlaLeuCysAsnValLeuIleGlyPhePheTyrGlyAsnMetTyrCysSerIleLu

CTTCATGACCTGCCTCAGTGTGCAGAGGTATTGGGTCATCGTGAACCCCATGGGGCACTC   600
uPheMetThrCysLeuSerValGlnArgTyrTrpValIleValAsnProMetGlyHisSe

CAGGAAGAAGGCAAACATTGCCATTGGCATCTCCCTGGCAATATGGCTGCTGACTCTGCT
rArgLysLysAlaAsnIleAlaIleGlyIleSerLeuAlaIleTrpLeuLeuThrLeuLe

GGTCACCATCCCTTTGTATGTCGTGAAGCAGACCATCTTCATTCCTGCCCTGAACATCAC   720
uValThrIleProLeuTyrValValLysGlnThrIlePheIleProAlaLeuAsnIleTh
```

FIG. 11A

```
GACCTGTCATGATGTTTTGCCTGAGCAGCTCTTGGTGGGAGACATGTTCAATTACTTCCT
rThrCysHisAspValLeuProGluGlnLeuLeuValGlyAspMetPheAsnTyrPheLe

CTCTCTGGCCATTGGGGTCTTTCTGTTCCCAGCCTTCCTCACAGCCTCTGCCTATGTGCT   840
uSerLeuAlaIleGlyValPheLeuPheProAlaPheLeuThrAlaSerAlaTyrValLe

GATGATCAGAATGCTGCGATCTTCTGCCATGGATGAAAACTCAGAGAAGAAAAGGAAGAG
uMetIleArgMetLeuArgSerSerAlaMetAspGluAsnSerGluLysLysArgLysAr

GGCCATCAAACTCATTGTCACTGTCCTGGGCATGTACCTGATCTGCTTCACTCCTAGTAA   960
gAlaIleLysLeuIleValThrValLeuGlyMetTyrLeuIleCysPheThrProSerAs

CCTTCTGCTTGTGGTGCATTATTTTCTGATTAAGAGCCAGGGCCAGAGCCATGTCTATGC
nLeuLeuLeuValValHisTyrPheLeuIleLysSerGlnGlyGlnSerHisValTyrAl

CCTGTACATTGTAGCCCTCTGCCTCTCTACCCTTAACAGCTGCATCGACCCCTTTGTCTA  1080
aLeuTyrIleValAlaLeuCysLeuSerThrLeuAsnSerCysIleAspProPheValTy

TTACTTTGTTTCACATGATTTCAGGGATCATGCAAAGAACGCTCTCCTTTGCCGAAGTGT
rTyrPheValSerHisAspPheArgAspHisAlaLysAsnAlaLeuLeuCysArgSerVa

CCGCACTGTAAAGCAGATGCAAGTACCCCTCACCTCAAAGAAACACTCCAGGAAATCCAG  1200
lArgThrValLysGlnMetGlnValProLeuThrSerLysLysHisSerArgLysSerSe

CTCTTACTCTTCAAGTTCAACCACTGTTAAGACCTCCTATTGAGTTTTCCAGGTCCTCAG
rSerTyrSerSerSerSerThrThrValLysThrSerTyr

ATGGGAATTGCACAGTAGGATGTGGAACCTGTTTAATGTTATGAGGACGTGTCTGTTATT  1320

TCCGGATCCAGATCTTATTAAAGCAGAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

AAAGCAATAGCATCACAAATTTCACAAATAAAGC                            1414
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FIG. 11B

FIG.12

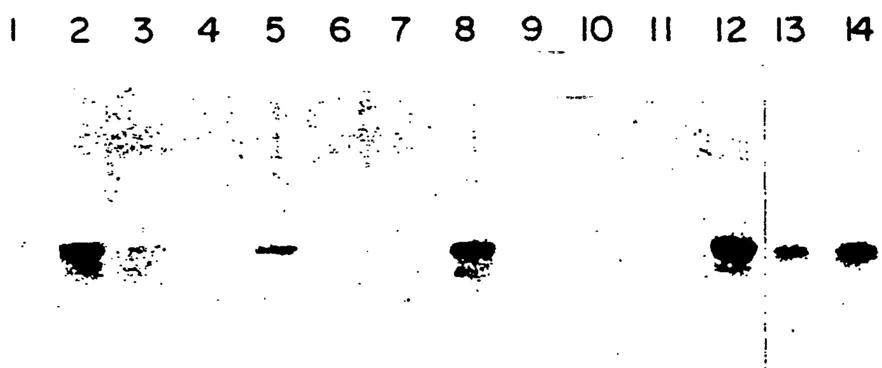

FIG.13